

## In the Specification

Please replace the last paragraph on page 15 with the following paragraph:

The comparison of sequences and determination of percent identity and similarity between two sequences can be accomplished using a mathematical algorithm.

(*Computational Molecular Biology*, Lesk, A. M., ed., Oxford University Press, N.Y., 1988; *Biocomputing: Informatics and Genome Projects*, Smith, D. W., ed., Academic Press, N.Y., 1993; *Computer Analysis of Sequence Data, Part 1*, Griffin, A. M., and Griffin, H. G., eds., Humana Press, N.J., 1994; *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, M. and Devereux, J., eds., M Stockton Press, N.Y., 1991). In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman and Wunsch (*J. Mol. Biol.*(48):444-453 (1970)) algorithm which has been incorporated into the GAP program in the GCG software package (~~available at <http://www.gcg.com>~~), using either a Blossom 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In yet another preferred embodiment, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package (Devereux, J., *et al*, *Nucleic Acids Res.* 12(1):387 (1984)) (~~available at <http://www.gcg.com>~~), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. In another embodiment, the percent identity between two amino acid or nucleotide sequences is determined using the algorithm of E. Myers and W. Miller (CABIOS, 4:11 - 17 (1989)) which has been incorporated into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4.